Structure of HTPL and alignment of Patched motifs. FIG. 1A HTPL-L (954 a.a.) HTPL-S (767 a.a.)

Patched

	78 240 125 97	152 313 199 171
α	* FISTNV AVQDLR YIQTRV FIRNNI	160 * EGN- LGMG neTDI- ngENI-
7.0	1 VLSSKIRYTFTTPDDIRSYTERGSRSEHEPL-VERKFFFPGDGYPISRFSIITAKARNS-NILDIRYLNEVVQVNDFISTNV 78 162 deeedleehYTPVGSPAKAERRFVQGHFTTnDSYRFSASRRSTEANFVSLLVVSYSD-SLLDPATFAEVSKLDGAVQDLR 240 47 NPLSDAVYLFTTPLGAQSKMERMSIHEKWPL-TDNNYIPGRAVTQSREIQVTALARNDSNILDPKFANAVYQLDKYIQTRV 125 22 NVVYSLLMIFGPYSYTERRIHDAWPL-VDGTFVAGRAVTQSREVQVAVVARSGGNILDRVFSNELKLMESFIRNNI 97 49 LRVDDPSYVFTPSDARWRREISVFNENWPL-DENKFLPGKSFEAKRFVNILIRAKDGGSIMRDNVLHEIEILNQWIMNNI 127	90 100 110 120 130 140 150 160 160 160 160 160 160 160 160 160 16
09	* ARNS-NILDI SYSD-SLLDD ARNDSNILDP ARSGGNILDR AKDGGSIMRDI	140 .* FFGTKIYLGFI HGRHPLYLTGI FGSEGGYIGSI
050	** ISRFSIITAK EANFVSLLVV QSREIQVTAL QSREVQVAVV	130 .* RIDLTYPTMT:SISFPAYN GFNITYPYFR: GINITYPTVR:
40	* ERKFFPGDGYE SYRFSASRRST DNNYIPGRAVT DGTFVAGRAVT ENKFLPGKSFE	120 * GQILRSNLHNS AWQVNKTLNLS HILSDLHNH QLASRLHQH
30	SRSEHEPL-V FVQGHFTTND SIHEKWPL-T I IHDAWPL-V	110 .* INCPVNQHYNGLCVPOPNPILY GGCPSNKHV- GRCANNDHI-
70	* *****. /LSSKIRYTFTPDDIRSYTERGSRSE leeedleehYTPVGSPAKAERRFVQG IPLSDAVYLFTPLGAQSKMERMSIHE IVVYSLLMIFGPYSYTERRIIHD IRVDDPSYVFTPSDARWREISVFNE	90 100* **** IIPVSGITLSFKDLCMRFCDINCPA VAREKGSQIQYQQVCARYRALCVPI RVLHNGHYYSYKNLCLQYKNGGCPE IVQFSNRTWSFADLCLAGPDGRCAN
10	* SKIRYTFTP: edleehYTP: SDAVYLFTP: 7SLLMIFGP:	90 * 7SGITLS1 IKGSQIQ7 INGHYYS3 INGRTWS1
1B motif	1 VLSS 162 dee6 47 NPLS 22 NVV3 49 LRVI	 79 TIPV 241 VARE 126 RVLH 98 TVQF
FIG. Patched	consensus HTPL-L gi 1825729 gi 1707052 gi 3892144	consensus 79 TIPVSGITLSFKDLCMRFCDINCPVNQHYNGQILRSNLHNSRIDLTYPTMTFFGTKIYLGPNFGGVKLDPNPGN- 152 HTPL-L 241 VAREKGSQIQYQQVCARYRALCVPPNPILYAWQVNKTLNLSSISFPAYNHGRHPLYLTGFFGGYILGGSLGMg 313 gi 1825729 126 RVLHNGHYYSYKNLCLQYKNGGCPSNKHVHILSDLHNHGFNITYPTYRFGSEGGYIGSSLGGVTVMKGeneTDI- 199 gi 1707052 98 TVQFSNRTWSFADLCLAGPDGRCANNDHIQLASRLHQHGINITYPTVRLSDKSAYIASALGGVKLAKGANGENI- 171 gi 3892144 128 SIPTDD1kFNLTYQDLCLSY-DWVCGANEHIQ-MLLRRNDVNQILDLHFPRGGTKDTPVYLGGIFGDVQFFQNGT- 200

FIG. 1B

Patched motif (Continued)

226 3926 273 246	2 4 5 9 3 4 5 2 8 3 4 5 2 8 4 5 5 5 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5	370 529 417 390 434	416 571 468 450 514
* · · · · · · · · · · · · · · · · · · ·	kn	* FFDF LFCY FFAE LLLTE	*
230 240* * -ELVRNGLTLTPFFVVGFA 1EFEATSVTVIPVFHLAYI -ELKRNADTLIPRFIISIT -ELKRNAERLAPKFIGAFV -GLDENAKAFVPNFVVSFF	. 1 . 1 . 1 . 1 . 1 . 1 . 1 . 1 . 1 . 1	390 IYTAVAI IYTGTTL VYTGVAI IYTMCAL	70
230 NGLT FSVT NADT	310 	390 	4 • 1 1 1 1 1
··*· SLVRI SFEA: SLKRI SLNRI	**. APFL APFL APFL (PFL)	··*· IQLF(VQCF(VQIF(IQFF(
220 LED1 LSRq11 LAD1 LSD1	300 SIVCVI IIVANS DIVGVI DIIAVI	380 TPTPE. SSFRSV TTIPAV TTIPAV	460 plpscq fnylss
.90 220 230 240 240*	FN F	AH AH CH	
TESD VVHF VFHS YFHS	* LGFR IGVP MGMP LEIQ LGVR	* FGIG LYTG FGVG FGVG	GSAK FPFG GSVP GSQP
210 . Q-VT KKIE KKIE S-IT T-LS	290 . LLEW LLLEH FLSL MLTY	370 INVLSF INVLSF IDVLSF IDALSF	450
.* D-HI L-AL P-YI AKYI D-VI	·*·· SAFG SGFG TGVG SAMG	.* TELT TEST TALT	. * O.R. F.K. - EO.R. V.K. kloo
90 200 . * WELSLFDYLENEYASD WLTHLLDQFTNIKNIL WELELGRMLTQYPEDP WEREFKNKMDEYKKQA FSYALETFLNQVYSSD	0 MAIV LAVV IAIL MGIA	SITI SILL SILL SILL	S Ln Eads
200 ZLENE ZFTNI ALTQY KMDEY	28(LTPLA ISAFI 7SAG: SNAGN	360 EAGPS CAAVS DAAVS DAAVS	0 440 * -AVDAAETESP -LKKADPKWPS -AVSAEKKTSLSt -AVTYSSTSPLn- qLVDISKMNEEad
*. ILED ILGRA ILGRA IFKNI	*. LGVI LGVV LGVV LGVS	GEVLE GEVLE SNVYS GECLAI AECMAL SKTLS	* DAAH KADDI SAEH TYSK
.90 . WELE WELE WERE		.50 RMGE RMGE RRGE	
* DSKE QSKQ TSGE VSGL	260 2 * SLHIDWVRSKPDCIRNKM SFSIDWVLSKP SGYIDWVVTKP	* SVKK DIRE TVHE	* LR CW LIE- TRP-
···· EVEE EYDV EMSY EISY	 IDWV IDWV IDWV	TRSL TRSL NLAG SRTH DRNL SKSL	HSLF HSLF NSLF HSLF HCLF
180 RDPEEV FHPEEM FYPNEI	260 GSLH GSFS GSGY SATK	340 WQRT' WHKT' VRRT' KKRT' WHQT	420 MKGR ASGR EQGL
170 180 1 * * * IKSVKAIVLYYRLKRDPEEVEEDSKE LLRAKAMRLLYYLKTEDPEYDVQSKQ LASAKAWFMIYHLKFHPEEMSYISGE IVEATAWLLIYQLKFYPNEISYVSGI LSDAKLTQLFYFLKQDQKMVEEYSSK	*	330 340 3 * **** AIGVDDMFLMVHAWQRTTRSLSVKK GVGVDDMFIMISAWHKTNLAGDIRE AVGVDNMFLMVAAVRRTSRTHTVHE AVGTDNMFLMVASLKRTDRNLKYDQ ipaigiddmflmnacwdQTSKSLSVPE	··*· skyei skrei kkhei krhei
170 KAIVLYYY KAWFMILY KAWFMIYY TAWLLIY	250 SILTSVRLA AVTSCFRF- STLCSLSFI SVLCSIVTI	OMEIN OMEIN OMEIN OMEIN	.0 * IAIDGKR] IALDGKR] AALAMKH] AVYTRI]
170 \ VKAIV AKAMR AKAWF	250 'SILTS' 'AVTSC' 'STLCS' 'SULCS' 'SULCS' 'ALVSS	330 .GVDDM: .GVDDM: .GTDNM:	410 "AAIMA "GAFMA "AACLA "CAILV
•	250 260 2 * *** ILVTFSILTSVRLAS-GSLHIDWVRSKP LIILFAVTSCFRFDCIRNKM LLIVFSTLCSLSFID-GSFSIDWVLSKP ILVCFSVLCSIVTIK-GSGYIDWVVTKP	330 340 3 * **** AIGVDDMFLMVHAWQRTTRSLSVKK GVGVDDMFIMISAWHKTNLAGDIRE AVGTDNMFLMVAAVRRTSRTHTVHE AVGTDNMFLMVASLKRTDRNLKYDQ qipaigiddmflmnacwdQTSKSLSVPE	410 420 4 * *** QLTFFAAIMAIAGKYEMKGRHSLFLR NITCFGAFMALDGKREVVCLCW QITFFAACLALAMKHEASGRNSLFLIE QLTFFCAILVYYTRIEEQGLHSIWLRP
153 - 314 q 200 - 172 - 201 -	227 I 393 L 274 L 247 I 275 V	96	71 (30] 18 (35 (
0 0 4	0 4	0 4	0 2 4
su 57 70 21	α <u>υ</u> ΓΟ Γ Ο	su 57 70 21	su 57 70 21
consensus HTPL-L gi 182572 gi 170705 gi 389214	consensus HTPL-L gi 182572 gi 170705 gi 389214	consensus HTPL-L gi 182572 gi 170705 gi 389214	consensus HTPL-L gi 182572 gi 170705 gi 389214
	ž E 3,,, 3,	, C 0. 0. 0.	2 - 3, 5, 5,

81/7

FIG. T

FIG. 1B

		552	709	607	009	671
640	*:	FLYSFISE	YLKGNS	-YYQKELE	-VSEEIHK	YLSELNAE
630	: :: *:	KFWLRDYEN	EFWLDAYVQ	QFWLFEMER	QFWLREMQ-	VFFLLEYLN
620	*	ITPYAMGKNST	INVY - VDKNLT	SKHAIGMESV	ICKVAIGDDSV	ITQYTLGREGT
610	· · · · * · · · · · · · * · · · · · · ·	SLNEMVDEFEN	KLENCTKIFER	RVHAMVLDFAT	NMDKMASTFAN	ILKVVSAFEN
009	*:	PDLTNPENRDE	VDYWDKDVRQI	PDLRNHTSRD	PDLRDPVERIN	PNLTISENRN
		LQVTVFVNNP	PRVMVIVTKK	QQVQIVINNA	ASLQIVVSNP	AQLHVAVLNP
580	*	LLREKHVWPYG	VEENYFSDYG	KLLEKYFWKYG	VVLekhywhyg	SDI-KHFWRIG
570	***********	476 FLKDSPLVEYLRLREKHVWPYGLQVTVFVNNPPDLTNPENRDRLNEMVDEFENTPYAMGKNSTKFWLRDYENFLYSFISE 555	633 ASDDSYITPYFNVEENYFSDYGPRVMVIVTKKVDYWDKDVRQKLENCTKIFEKNVY-VDKNLTEFWLDAYVQYLKGNS	gi 1825729 529 LVEDSYAIPHYRLLeKYFWKYGQQVQIVINNAPDLRNHTSRDRVHAMVLDFATSKHAIGMESVQFWLFEMER-YYQKELE 607	gi 1707052 523 LVDDSYATPHYRVLeKHYWHYGASLQIVVSNPPDLRDPVERINMDKMASTFANCKVAIGDDSVQFWLREMQVSEEIHK 600	gi 3892144 593 VTNDHYIAKYFSDI-KHFWRIGAQLHVAVLNPPNLTISENRNELLKVVSAFENTQYTLGREGTVFFLLEYLNYLSELNAE 671
		476	633	529	523	593
		consensus	HTPL-L	1825729	1707052	3892144
		COI	HTI	gi	gi	gi

consensus HTPL-L	556 710		660 * *. VFL-KSPGFSHW	670 * VVGDLVWDN-:	680 * KTDYETTIVK NISSSNEIIS	690 *. KFRFTTGGKDI SRGF-TOTTDV	700 *. .STWTDRTRL.	/ I U *. .KTWRGVADEY. .FOI.RRIA-EU	 PDFN 633
gi 1825729	608	gi 1825729 608 VQIID-SSFYGLLHHFL-ASKTNNPLAEDIYWGPmPDDDNGTMVKSFRFILGMKDLVTTMDQTDATMSFREVAARWPEFN 685	HFL-ASKTNNPI	AEDIYWGPm	PDDDNGTMVK	SFRFILGMKDI	JVTTMDQTDAJ	MSFREVAARW	PEFN 685
gi 1707052	601	gi 1707052 601 IQYDN-EKFYDHAAQYI-YSDMSQPWVVDVVWGRNNNSERIIKTFRFMIGMRDISTTTKQTEATNTFREIASRFEQYN 676	2YI-YSDMSQPW	TVVDVVWG:	RNNNSERIIK	TFRFMIGMRD:	ISTTTKQTEAJ	INTFREIASRF	TOYN 676
gi 3892144	672	gi 3892144 672 VEDTERLWKTKLNSWLK-YTGGSTQWASNLKINKTDGSFQAFRFQIALKNFVEPNDHKHAAQLLRDIADHQP-FN 744	VLK-YTGGSTQW	ASNLKIN	KTDGSFQ	AFRFQIALKNI	PVEPNDHKHAA	QLLRDIADHQ	P-FN 744

		386	332	138	729	324
800	*:	FVITVSI 6	LWVTFAI 8	LWVALAC 7	FWVAVTI 7	FVIFVSI 8
790	*	FLFI PNPNTV	LLLIPYPLCS	VLFIPQPMCS	ALLI PQPVCS	FLLVPSLPSG
780	:	WILICMAVVC	VASAAMFIVS	TALLVMIVIA'	VAVACMLVIS	ISLLCMAVVS
770		AFFLDQILSIGPTTIQSIIWTLICMAVVCFLFIPNPNTVFVITVSI 686	FIYFDQYAAILEDTVRNVLVASAAMFIVSLLLIPYPLCSLWVTFAI 832	WMFTDQYIIIIPNTVQNIIIALLVMIVIAVLFIPQPMCSLWVALAC 738	WLFTDQYALVVPNTMQDIIVAVACMLVISALLIPQPVCSFWVAVTI	ILPATIONVV
160	*:	AFFLDQILS	FIYFDQYAA	WMFTDQYII	WLFTDQYAL	Lafpfadoylli
750		! ! ! !	 		; ; ; ; ; ; ;	scyaqknipk]
740	*:	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1			1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	kilndfissh
730	*	634 VTVFDED	780 LMVYNQA	686 VTTFMPI	677 VTTYMPL	745 VVVYHEVsfgnrkilndfisshscyaqknipklaFPFADQYLIILPATIQNVVISLLCMAVVSFLLVPSLPSGFVIFVSI 824
		consensus 6	HTPL-L 7	gi 1825729 6	gi 1707052 6	gi 3892144 7

FIG. 1B

Patched motif (Continued)

Structure of the HTPL gene (Chr. 10p12.1)

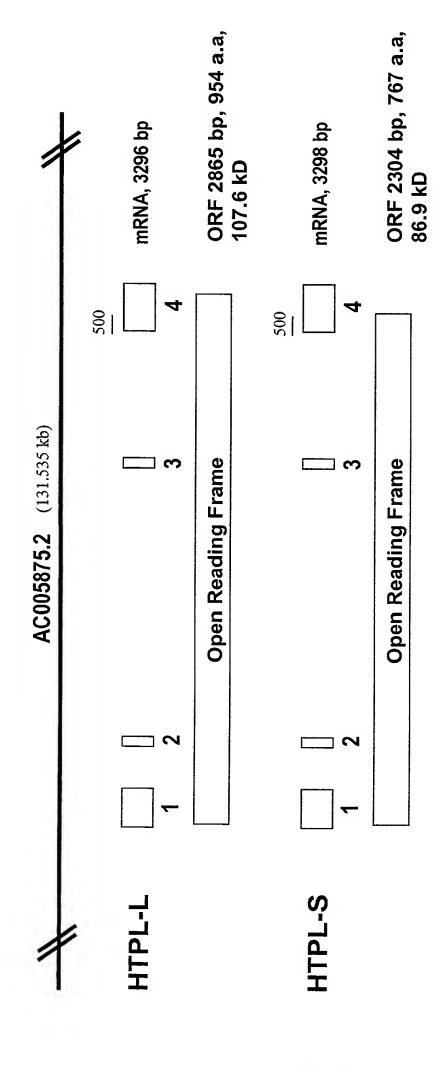


FIG.

HTPL-L

nt: SEQ ID NO: 1 aa: SEQ ID NO: 3

CAG	GAAA(CCGT	CTGG'	TGGG2	ATCT(CCGC	AGCT(GCTT'	ITCA(CCTG	CTGT:	TCCTC	52
CTG	CGCT'	FCCT	AAGA	GGAA(GAAT(W ' GG G'				6 95
									P CCC				19 134
												E GAA	
									Q CAG			P CCG	45 212
									E GAA			G GGA	58 251
									L CTG				71 290
												A GCA	
												P CCG	
													110 407
												L CTG	123 446

S 0 W L G 136 W 0 G Α TCC CGC ACC TTC CAG TGG CTG GGG TGG CAG GTG GGC GCG 485 Η Ρ F W Ι \mathbf{L} \mathbf{L} Α Ρ L Τ Μ L 149 CAC CCC TGG ATC TTC CTG CTG GCG CCC TTG ATG CTG ACA 524 Α A L G T G F L Y \mathbf{L} Р K D 162 GCC GCG CTG GGC ACC GGC TTC CTG TAC CTA CCC AAG GAC 563 Ε Ε E D \mathbf{L} Ε Ε Η Y T Ρ G V 175 GAA GAG GAA GAC CTA GAG GAG CAT TAC ACC CCT GTG GGG 602 S P Α K Α E R F R V 0 G Η 188 AGC CCG GCC AAG GCG GAG CGG CGC TTC GTG CAG GGC CAT 641 F T T N D S Y R F S A S R 201 TTC ACC ACC AAC GAC TCC TAC CGC TTC TCC GCC TCC AGG 680 R S T E A V N F S L L V V 214 AGG AGC ACC GAA GCC AAT TTC GTC TCG CTT CTG GTG GTC 719 S Y S D S L L D P Α \mathbf{T} F Α 227 TCC TAC AGC GAC TCA CTG CTG GAC CCA GCT ACC TTT GCA 758 \mathbf{E} V S K L G D Α V Q D L R 240 GAA GTC AGC AAA CTG GAC GGC GCG GTG CAG GAT CTG CGC 797 V Α R \mathbf{E} K G S 0 I Q Y Q Q 253 GTG GCG CGG GAA AAG GGA AGC CAG ATC CAG TAC CAG CAG 836 Α Y R R Α L C V Ρ Ρ Ν 266 GTG TGC GCG AGG TAC AGG GCG CTC TGC GTG CCC CCC AAC 875 Ρ I \mathbf{L} Υ A W Q V T L Ν K N 279 CCG ATC CTG TAC GCC TGG CAG GTG AAC AAA ACG CTC AAC 914 L S Ι S F P Α Y N Η G R 292 CTG AGC AGC ATC TCC TTC CCC GCC TAC AAC CAC GGC AGG 953 Η Y \mathbf{L} Τ G F F G G Y Ι 305 CAT CCC CTC TAC CTG ACC GGC TTC TTC GGA GGA TAC ATC 992

FIG. 3

L G G S L G Μ G Q \mathbf{L} L L R 318 TTG GGG GGC AGC CTA GGA ATG GGC CAG TTA CTC CTG CGG 1031 Α K Α M R L L Y Y \mathbf{L} 331 K E GCC AAA GCC ATG CGG CTG CTG TAC TAC CTG AAG ACC GAG 1070 Ρ D E Y D V Q S K Q Τ W L 344 GAC CCT GAG TAC GAC GTG CAG AGC AAG CAG TGG CTC ACC 1109 Η \mathbf{L} L D F T Q N Ι K N Ι $\mathbf{L}_{\mathbf{L}}$ 357 CAT TTG CTC GAT CAA TTT ACC AAC ATT AAG AAC ATC TTG 1148 A \mathbf{L} K K Ι E V V Η F T L S 370 GCC TTG AAA AAA ATT GAG GTA GTC CAC TTT ACA TCG CTT 1187 S R Q L Ε F E A T S V V 383 TCC AGA CAA CTG GAA TTT GAG GCA ACT TCT GTG ACT GTG 1226 Ι P V F Η \mathbf{L} Α Y Ι L I L Ι 396 ATC CCT GTG TTT CAC CTG GCA TAC ATT CTC ATC ATT CTG 1265 F Α V T S C F R F D C Ι R 409 TTT GCA GTC ACA TCA TGC TTT AGG TTT GAC TGC ATA CGA 1304 NK M C V F Α A G V Ι S Α 422 AAC AAA ATG TGT GTT GCG GCC TTT GGA GTG ATT TCT GCT 1343 F \mathbf{L} Α V V S G F G L L L Η 435 TTC TTG GCA GTG GTG AGC GGC TTT GGC CTG CTG TTG CAC 1382 Ι G V Ρ F V I Ι V A N S Ρ 448 ATT GGG GTG CCA TTT GTC ATC ATA GTT GCC AAT TCA CCA 1421 F L I G L V G V D D Μ F I 461 TTT CTT ATT CTA GGT GTT GGG GTC GAT GAC ATG TTT ATC 1460 M Ι S Α W Η K T N L Α G D 474 ATG ATT TCT GCC TGG CAT AAG ACC AAC CTT GCA GGT GAC 1499 I R Ε R M S N V Υ S K A Α 487 ATA CGA GAG CGG ATG TCC AAT GTC TAT TCA AAA GCG GCA 1538

FIG. 3

S Ι T Ι Т T Ι Τ Ν Ι 500 L Α GTG TCT ATT ACA ATC ACC ACC ATC ACT AAC ATC CTG GCC 1577 L Υ Τ G I M S S F R S Q 513 TTA TAT ACA GGG ATT ATG AGC TCT TTT AGG TCC GTA CAA 1616 C CΙ Y T G T T L L C F 526 TGT TTT TGC ATC TAT ACA GGA ACG ACC CTG TTA TTT TGC 1655 Y F Y Ν Ι T C F G Α F М Ά 539 TAT TTT TAT AAC ATC ACG TGT TTT GGA GCA TTT ATG GCC 1694 L D G K R E V V C L C W L 552 TTG GAT GGT AAA AGA GAA GTA GTC TGC CTA TGC TGG TTG 1733 K K A D P K W Ρ S F K K F 565 AAA AAG GCT GAC CCA AAA TGG CCC TCA TTT AAA AAG TTC 1772 C C F P F G S V Ρ D E G Η 578 TGC TGT TTC CCA TTT GGT TCT GTC CCA GAT GAA CAT GGA 1811 T D I Η P Μ S L F F R D Y 591 ACT GAT ATC CAT CCA ATG AGT TTG TTT TTT AGA GAC TAT 1850 F G P F L T R S S E K Y F 604 TTT GGC CCC TTT CTC ACA AGG AGT GAG TCC AAG TAT TTT 1889 V F Ι Y V \mathbf{L} Y Ι I S S Ι 617 GTA GTC TTT ATA TAT GTT TTG TAC ATC ATA AGC AGT ATA 1928 Y G C F Η V O E G \mathbf{L} D L R 630 TAT GGG TGT TTC CAT GTG CAG GAA GGT TTA GAC CTT CGA 1967 N L Α S D D S Y Ι T P Y F 643 AAT CTG GCA AGT GAC GAT TCC TAC ATC ACA CCA TAT TTT 2006 N V Ε \mathbf{E} Ν Y F S D Y G Ρ R 656 AAC GTA GAG GAG AAT TAT TTT TCA GAT TAT GGT CCC AGG 2045 V M I V T K K V D Y W D 669 GTT ATG GTT ATT GTT ACT AAA AAA GTT GAC TAC TGG GAT 2084

FIG. 3

K	D	V	R	Q	K	L	E	N	С	${f T}$	K	I	682
AAA	GAT	GTT	AGG	CAA	AAA	CTG	GAA	AAC	TGT	ACT	AAA	ATT	2123
F	E	K	N	V	Y	V	D	K	N	L	${f T}$	E	695
TTT	GAA	AAA	AAT	GTC	TAT	GTA	GAT	AAA	AAT	CTT	ACA	GAG	2162
													708
TTT	TGG	TTA	GAT	GCA	TAT	GTG	CAA	TAT	TTA	AAA	GGT	AAC	2201
													721
AGC	CAA	GAT	CCT	AAT	GAG	AAG	AAT	ACT	TTT	ATG	AAC	AAT	2240
I	P	D	F	L	S	N	F	P	N	F	Q	H	734
ATT	CCT	GAT	TTT	TTA	AGC	AAT	TTT	CCA	AAT	TTT	CAG	CAT	2279
													747
GAT	ATT	AAT	ATT	TCT	TCA	TCA	AAT	GAA	ATC	ATT	TCT	TCC	2318
R	G	F	I 	Q	T	\mathbf{T}	D	V	S	S	S	A	760
CGG	GGC	TTC	A'I'T	CAG	ACA	ACA	GAT	GTT	TCT	TCC	TCA	GCC	2357
T.F	TZ	¥2		~			_	_	_				
K	K	K	J. (12)	Т	L	F	Q	_L	R	R	I	A	773
AAA	AAG	AAA	ATA	TTG	J.J.A	T.T.C	CAA	TTA	CGA	CGC	ATA	GCT	2396
E7	D	a	_		ъ	-	3.5				_	_	
E	D	C	Q	I	P	L	M	V	Y	N	Q	A	786
E GAA	D GAC	C TGT	Q CAA	I ATT	P CCC	L CTA	M ATG	V GTG	Y TAT	N AAC	Q CAG	A GCA	786 2435
GAA	GAC	TGT	CAA	ATT	CCC	CTA	ATG	GTG	TAT	AAC	CAG	GCA	2435
GAA F	GAC I	TGT Y	CAA F	ATT D	CCC Q	CTA Y	ATG A	GTG A	TAT	AAC L	CAG E	GCA D	2435 799
GAA F	GAC I	TGT Y	CAA F	ATT D	CCC Q	CTA Y	ATG A	GTG A	TAT	AAC L	CAG E	GCA D	2435
GAA F TTT	GAC I ATA	TGT Y TAT	CAA F TTT	D GAT	CCC Q CAG	CTA Y TAT	ATG A GCT	GTG A GCA	TAT I ATA	AAC L TTA	CAG E GAA	GCA D GAC	2435 799 2474
GAA F TTT T	GAC I ATA V	TGT Y TAT R	CAA F TTT N	D GAT V	CCC Q CAG L	CTA Y TAT V	ATG A GCT A	GTG A GCA S	TAT I ATA A	AAC L TTA A	CAG E GAA M	GCA D GAC F	2435 799 2474 812
GAA F TTT T	GAC I ATA V	TGT Y TAT R	CAA F TTT N	D GAT V	CCC Q CAG L	CTA Y TAT V	ATG A GCT A	GTG A GCA S	TAT I ATA A	AAC L TTA A	CAG E GAA M	GCA D GAC F	2435 799 2474
GAA F TTT T ACT	GAC I ATA V GTT	TGT Y TAT R AGA	F TTT N AAT	D GAT V GTA	CCC Q CAG L TTG	Y TAT V GTT	ATG A GCT A GCA	GTG A GCA S TCA	I ATA A GCA	AAC L TTA A GCT	E GAA M ATG	GCA D GAC F TTC	2435 799 2474 812 2513
GAA F TTT T ACT	GAC I ATA V GTT V	Y TAT R AGA	F TTT N AAT	D GAT V GTA	CCC Q CAG L TTG	Y TAT V GTT	ATG A GCT A GCA	GTG A GCA S TCA	I ATA A GCA	AAC L TTA A GCT	CAG E GAA M ATG	GCA DGAC FTTC	2435 799 2474 812 2513
GAA F TTT T ACT	GAC I ATA V GTT V	Y TAT R AGA	F TTT N AAT	D GAT V GTA	CCC Q CAG L TTG	Y TAT V GTT	ATG A GCT A GCA	GTG A GCA S TCA	I ATA A GCA	AAC L TTA A GCT	CAG E GAA M ATG	GCA DGAC FTTC	2435 799 2474 812 2513
GAA F TTT T ACT I ATT	GAC I ATA V GTT V GTT	Y TAT R AGA S TCC	F TTT N AAT L TTA	D GAT V GTA L TTG	CCC Q CAG L TTG L TTA	Y TAT V GTT I ATC	ATG A GCT A GCA P CCT	GTG A GCA S TCA Y TAT	I ATA A GCA P CCA	L TTA A GCT L TTG	CAG E GAA M ATG C TGT	GCA DGAC FTTC	2435 799 2474 812 2513 825 2552
GAA F TTT T ACT I ATT	GAC I ATA V GTT V GTT	Y TAT R AGA S TCC	F TTT N AAT L TTA	D GAT V GTA L TTG	CCC Q CAG L TTG L TTA	Y TAT V GTT I ATC	ATG A GCT A GCA P CCT	GTG A GCA S TCA Y TAT S	I ATA A GCA P CCA	AAC L TTA A GCT L TTG	CAG E GAA M ATG C TGT	GCA DGAC FTTC STCC	2435 799 2474 812 2513 825 2552
GAA F TTT T ACT I ATT	GAC I ATA V GTT V GTT	Y TAT R AGA S TCC	F TTT N AAT L TTA	D GAT V GTA L TTG	CCC Q CAG L TTG L TTA	Y TAT V GTT I ATC	ATG A GCT A GCA P CCT	GTG A GCA S TCA Y TAT S	I ATA A GCA P CCA	AAC L TTA A GCT L TTG	CAG E GAA M ATG C TGT	GCA DGAC FTTC STCC	2435 799 2474 812 2513 825 2552
GAA F TTT T ACT I ATT L TTG	GAC I ATA V GTT V GTT W TGG	Y TAT R AGA S TCC V GTG	F TTT N AAT L TTA T ACT	D GAT V GTA L TTG F TTT	CCC Q CAG L TTG L TTA A GCT	Y TAT V GTT I ATC	ATG A GCT A GCA P CCT G GGT	GTG A GCA S TCA Y TAT S TCT	I ATA A GCA P CCA V GTG	AAC L TTA A GCT L TTG I ATT	E GAA M ATG C TGT V GTA	GCA DGAC FTTC STCC GGGG	2435 799 2474 812 2513 825 2552 838 2591
GAA F TTT T ACT I ATT L TTG	GAC I ATA V GTT W TGG T	Y TAT R AGA S TCC V GTG	F TTT N AAT L TTA T ACT	D GAT V GTA L TTG F TTT	CCC Q CAG L TTG A GCT A	Y TAT V GTT I ATC I ATC	ATG A GCT A GCA P CCT G GGT	GTG A GCA S TCA Y TAT S TCT	I ATA A GCA P CCA V GTG	AAC L TTA A GCT L TTG I ATT	CAG E GAA M ATG C TGT V GTA L	GCA DGAC FTTC STCC GGGG	2435 799 2474 812 2513 825 2552

S	T	S	ľΛľ	Τ.	N	L	V	I	С	${ m T}$	G	F	864
TCC	ATA	TCC	ATG	ATT	AAT	CTT	GTC	ATT	TGT	ACA	GGG	TTT	2669
													877 2708
												E GAG	
												A GCA	
												A GCG	916 2825
												F TTT	929 2864
												F TTT	942 2903
												* TGA	955 2942
ATA	CCAC	CTAAC	CAAGT	CAAA	AGACO	CAATT	CTAC	TAAE	CCTC	FATTO	GCCC1	TATTC	2994
CAAT	CTGA	\TTT	TTTT	AATO	GCAC1	CATTA	AGAZ	ATAG1	CAAC	CAAAC	CTACI	GGGA	3046
GGC	CAAAG	GTGGC	GTGGA	ATCAC	CCTGA	AGGTC	CAAGA	ATTC	CGAGA	ACCAC	GCCTC	GCCA	3098
ACAT	GGT	SAAAC	CCTCG	BACAC	CTACT	GAAA	ATAC	CAAAA	ATTA	ATCCF	AGGCA	ATGGT	3150
GGCG	FTGCA	ACCTA	raat <i>i</i>	CCCA	AGCTA	ACCTO	GGAG	GCTG	BAGGC	CAGGA	GAAT	CGCT	3202
TGAA	CCTG	GGAG	SATGO	SAGGI	TGCA	GTGA	GCTG	GAGI	GCAC	CCAGO	GCACI	CCAG	3254
CCTG	GGTG	BACAA	AGAAT	GAGA	CTCC	CGTCT	'CAGA	AAAA	AAAA	AAA			3296

HTPL-S

nt: SEQ ID NO: 4 aa: SEQ ID NO: 6

CAG	GAAA	CCGT	CTGG'	TGGG:	ATCT	CCGC	AGCT	GCTT'	TTCA	CCTG	CTGT'	TCCTC	52
CTG	CGCT'	TCCT	AAGA	GGAA	GAAT(W T				6 95
K	P	R	Р	G	P	E	Q	K	P	K	L	${f T}$	19
AAG	CCC	AGG	CCG	GGG	CCG	GAG	CAG	AAG	CCC	AAG	CTC	ACC	134
K	P	D	S	A	Т	G	P	Q	M	Y	Q	E	32
AAA	CCG	GAC	TCT	GCC	ACC	GGG	CCG	CAG	TGG	TAC	CAG	GAA	173
												P	
TCT	CAG	GAA	TCG	GAG	TCG	GAA	GGC	AAG	CAG	CCA	CCC	CCG	212
													58
GGA	CCC	CTG	GCA	CCC	CCG	AAA	TCC	CCC	GAA	CCC	TCA	GGA	251
P	L	A	S	E	Q	D	A	P	L	P	E	G	71
CCC	CTG	GCG	TCG	GAG	CAG	GAT	GCA	CCC	CTG	CCA	GAG	GGG	290
D	D	A	Р	P	R	P	S	M	L	D	D	A	84
GAC	GAT	GCA	CCC	CCC	CGG	CCG	TCG	ATG	CTG	GAC	GAT	GCA	329
													97
CCC	CGC	CTG	CCG	CTG	GAG	CTG	GAC	GAT	GCA	CCC	CTG	CCG	368
E	E	E	${f T}$	P	E	P	${f T}$	A	I	С	R	H	110
GAG	GAG	GAA	ACC	CCC	GAA	CCC	ACG	GCC	ATC	TGC	AGG	CAC	407
R	Н	R	С	Н	${f T}$	D	С	L	E	G	L	L	123
CGG	CAC	CGC	TGT	CAC	ACC	GAC	TGC	CTA	GAG	GGG	CTG	CTG	446
S	R	T	F	Q	M	L	G	W	Q	V	G	A	136
TCC	CGC	ACC	TTC	CAG	TGG	CTG	GGG	TGG	CAG	GTG	GGC	GCG	485

			I ATC										149 524
			G GGC										162 563
			D										175
GAA	GAG	GAA	GAC	CTA	GAG	GAG	CAT	TAC	ACC	CCT	GTG	GGG	602
			K AAG										188 641
			N AAC										201 680
			E GAA										214 719
			D GAC										227 758
			K AAA										240 797
			E GAA										253 836
												N AAC	
												N AAC	
												R AGG	
												I ATC	
													318 1031
						\mathbf{F}	IG.	4					

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14/18

Α Y Y L K Τ Ε 331 K Α Μ R L \mathbf{L} GCC AAA GCC ATG CGG CTG CTG TAC TAC CTG AAG ACC GAG 1070 D E Y D V S K Q Τ 344 Q W GAC CCT GAG TAC GAC GTG CAG AGC AAG CAG TGG CTC ACC 1109 Τ Η L L F N Ι K Ι \mathbf{L} 357 D Q Ν CAT TTG CTC GAT CAA TTT ACC AAC ATT AAG AAC ATC TTG 1148 Α L K K Ι \mathbf{F}_{i} V V Η F Т S T, 370 GCC TTG AAA AAA ATT GAG GTA GTC CAC TTT ACA TCG CTT 1187 S T S T V R 0 L E F E Α V 383 TCC AGA CAA CTG GAA TTT GAG GCA ACT TCT GTG ACT GTG 1226 Ρ V I I F Η L Α Y L Ι Ι L 396 ATC CCT GTG TTT CAC CTG GCA TAC ATT CTC ATC ATT CTG 1265 F Α V T S C F R F R D C Ι 409 TTT GCA GTC ACA TCA TGC TTT AGG TTT GAC TGC ATA CGA 1304 N K C V F G V Ι S Α M Α Α 422 AAC AAA ATG TGT GTT GCG GCC TTT GGA GTG ATT TCT GCT 1343 F \mathbf{L} Α V V S G F G L L L Η 435 TTC TTG GCA GTG GTG AGC GGC TTT GGC CTG CTG TTG CAC 1382 G V P F V V S P I Ι Ι A N 448 ATT GGG GTG CCA TTT GTC ATC ATA GTT GCC AAT TCA CCA 1421 F L Ι L G V G V D D M F I 461 TTT CTT ATT CTA GGT GTT GGG GTC GAT GAC ATG TTT ATC 1460 Ι S Α W K Τ Ν Α D 474 M Η L D ATG ATT TCT GCC TGG CAT AAG ACC AAC CTT GCA GAT GAC 1499 I R E V Y S K Α R M S N A 487 ATA CGA GAG CGG ATG TCC AAT GTC TAT TCA AAA GCG GCA 1538 Ι T I T T I T N Ι L Α 500 GTG TCT ATT ACA ATC ACC ACC ATC ACT AAC ATC CTG GCC 1577

FIG. 4

S S F V L Y T G Ι M R S 0 513 TTA TAT ACA GGG ATT ATG AGC TCT TTT AGG TCT GTA CAA 1616 Ι Y T G M T \mathbf{L} L F C 526 TGT TTT TGC ATC TAT ACA GGA ATG ACC CTG TTA TTT TGC 1655 Υ F Y Ι T C F G F Α N Α Μ 539 TAT TTT TAT AAC ATC ACG TGT TTT GGA GCA TTT ATG GCC 1694 K R E V V C L C L 552 TTG GAT GGT AAA AGA GAA GTA GTC TGC CTA TGC TGG TTG 1733 K K Α D Ρ K W Ρ S F K K F 565 AAA AAG GCT GAC CCA AAA TGG CCC TCA TTT AAA AAG TTC 1772 P F G S V Р D E G 578 H TGC TGT TTC CCA TTT GGT TCT GTC CCA GAT GAA CAT GGA 1811 T Ρ S F F R Y I Η Ι L D 591 ACT GAT ATC CAT CCA ATA AGT TTG TTT TTT AGA GAC TAT 1850 Ρ G F L Τ R S E S K Y F 604 TTT GGC CCC TTT CTC ACA AGG AGT GAG TCC AAG TAT TTT 1889 V V \mathbf{F} Ι Y V L Y I I S S Ι 617 GTA GTC TTT ATA TAT GTT TTG TAC ATC ATA AGC AGT ATA 1928 Y G C F Η V Q E G L D L R 630 TAT GGG TGT TTC CAT GTG CAG GAA GGT TTA GAC CTT CGA 1967 Ν L A S D D S Y Ι T Ρ Y F 643 AAT CTG GCA AGT GAC GAT TCC TAC ATC ACA CCA TAT TTT 2006 N V E E Ν Y F S D Y G P R 656 AAC GTA GAG GAG AAT TAT TTT TCA GAT TAT GGT CCC AGG 2045 V V M Ι V T K K V D Y D 669 GTT ATG GTT ATT GTT ACT AAA AAA GTT GAC TAC TGG GAT 2084 K D V Q K C R L E N T K Ι 682 AAA GAT GTT AGG CAA AAA CTG GAA AAC TGT ACT AAA ATT 2123 F E K V V N Y D K Ν L T Ε 695 TTT GAA AAA AAT GTC TAT GTA GAT AAA AAT CTT ACA GAG 2162

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16/18

F TTT	W TGG	L TTA	D GAT	A GCA	Y TAT	V GTG				K AAA	G GGT	N AAC	708 2201
S AGC	Q CAA	D GAT	P CCT	N AAT	E GAG	K AAG	N AAT	T ACT	F TTT	M ATG	N AAC	N AAT	721 2240
I ATT	P CCT	D GAT	F TTT	L TTA	S AGC	N AAT	F TTT		N AAT	F TTT	Q CAG	H CAT	734 2279
D GAT	I ATT	N AAT	I ATŢ	S TCT	S TCA	S TCA	N AAT	E GAA	I ATC	I ATT	S TCT	S TCC	747 2318
R CGG	G GGC	F TTC	I ATT	Q CAG		T ACA	D GAT		S TCT	S TCC	S TCA	A GCC	760 2357
K AAA	K AAG	K AAA	I ATA	L TTG	L TTA	F TTC	* TAA	TTA	ACGA	CGCAT	rage:	rgaag	768 2400
ACTGTCAAATTCCCCTAATGGTGTATAACCAGGCATTTATATATTTTGATCA								2452					
GTATGCTGCAATATTAGAAGACACTGTTAGAAATGTATTGGTTGCATCAGCA								2504					
GCTATGTTCATTGTTATTGTTAATCCCTTATCCATTGTGTTCCTTGT								2556					
GGGTGACTTTTGCTATTGGTTCTGTGATTGTAGGGGTTAACGGGTTTCATGGC								2608					
ATTO	CTGGA	\AAG'	[CAA]	CTTC	ATTO	CCATA	ATCC	ATGAT	[TAAT	CTTC	GTCA:	TTTGT	2660
ATAGGGTTTTCTTTCGATTTTCTGTACACATTTCCTATGCATTTGTTTCTA								2712					
GTTC	CTCA	ACCCI	rcag'i	CAAAC	CCAAA	AATC	CAGTT	rgago	GCATT	rgta:	CTT	CTAGG	2764
CTAC	CCCAC	GTGTT	TACAZ	AGTO	GCAAT	TTC	ACAZ	LAAT!	raggo	GTGT	rgtg:	TTTTA	2816
GCT	GCAGC	CGAAA	AGCAT	CACAT	CTTC	CAGA	ACATI	TTTT	TAAGA	ATTA	rgtt:	CTTG	2868
TTAT	GATA	ATTTC	GGGC	CAGCT	CATO	GCCI	'AAT'	TTTP	ATTCC	CAGTA	ATTCT	TTAAC	2920
CTTT	TTTT	GAAG	GTTI	TTTAT	GAAT	TATCO	CACTA	ACAA	AGTCF	AAGA	ACCA?	ATTCT	2972
AGAA	ATTCC	CTGAT	TGCC	CCTAT	TCCA	ATCI	GATT	TTTT	TAA	ATGCZ	ACTAT	TTAAG	3024
AATAGTCAACAAACTACTGGGAGGCCAAGGTGGGTGGATCACCTGAGGTCAA									3076				

GAATTCGAGACCAGCCTGGCCAACATGGTGAAACCTCGACACTACTGAAAAT	3128
ACAAAAATTATCCAGGCATGGTGGCGTGCACCTATAATCCCAGCTACCTGGG	3180
AGGCTGAGGCAGGAGATCGCTTGAACCTGGGAGATGGAGGTTGCAGTGAGC	3232
TGGAGTGCACCAGGCACTCCAGCCTGGGTGACAAGAATGAGACTCCGTCTCA	3284
GAAAAAAAAAA	3298

HTPL tissue distribution by RT-PCR

brain
heart
skeletal muscle
bone marrow
lung
liver

kidney colon testis

placenta

uterus

marker